IN THE CLAIMS

Amend claims 1 and 9 as follows:

D1

1. (Amended) Sequence of a human beta2-adrenergic receptor gene, the sequence comprising at least one base substitution at one or more positions selected from the group consisting of positions 159, 245, 565, 934, 1120, 1221, 1541, 1568, 1839, 2110, 2640 and 2826.

D2

9. (Amended) A method for determining dispositions to diseases wherein the DNA of a proband is extracted and analyzed for sequence variations, and is compared with at least one similarly analyzed reference DNA sequence, wherein the reference DNA sequence comprises a base substitution at one or more positions selected from the group consisting of positions 159, 245, 565, 934, 1120, 1221, 1541, 1568, 1839, 2110, 2640 and 2826, and wherein the method comprises the steps of:

hybridizing at least one pair of primers to genomic DNA comprising the beta2-adrenergic receptor gene under conditions suitable for performing PCR;

amplifying one or more genomic sequences by PCR;

analyzing the amplified sequences to discern differences between the proband and reference DNAs.

Please add the following new claims 34-42:

D3

34. (New) A human beta2-adrenergic receptor genomic DNA variant determined by the method of claim 9, wherein the variant comprises a base substitution at one or more positions of a reference DNA sequence, the positions being selected from the

group consisting of positions 159, 245, 565, 934, 1120, 1221, 1541, 1568, 1633, 1666, 1839, 2078, 2110, 2640 and 2826.

35 ~~34~~. (New) A variant of claim 34 comprising one or more base substitutions selected from the group consisting of:

(i) at position 159, T→A;

(ii) at position 245, A→G;

(iii) at position 565, G→A;

(iv) at position 934, G→A;

(v) at position 1120, G→C;

(vi) at position 1221, C→T;

(vii) at position 1541, C→T;

(viii) at position 1568, T→C;

(ix) at position 1633, A→G;

(x) at position 1666, C→G;

(xi) at position 1839, G→A;

(xii) at position 2078, C→T;

(xiii) at position 2110, C→A;

(xiv) at position 2640, G→C; and

(xv) at position 2826, G→A.

36. (New) The genomic DNA variant determined by the method of claim 9, wherein the variant comprises one or more substitutions selected from the group consisting of a T at position 1541, an A at position 1633, and a C at position 1666.

37. (New) The genomic DNA variant determined by the method of claim 9, wherein the variant comprises one or more substitutions selected from the group consisting of a C at position 1541, a G at position 1633, and a G at position 1666.

38. (New) The genomic DNA variant determined by the method of claim 9, wherein the variant comprises one or more substitutions selected from the group consisting of a T at position 1541, a G at position 1633, and a C at position 1666.

39. (New) The genomic DNA variant determined by the method of claim 9, wherein the variant comprises one or more substitutions selected from the group consisting of a T at position 1541, T at 1568, A at position 1633, and C at position 1666.

40. (New) The genomic DNA variant determined by the method of claim 9, wherein the variant comprises one or more substitutions selected from the group consisting of a C at position 1541, C at position 1568, G at 1633 and G at position 1666.

41. (New) The genomic DNA variant determined by the method of claim 9, wherein the variant comprises one or more substitutions selected from the group consisting of a T at position 1541, T at position 1568, G at 1633 and C at position 1666.

42. (New) The sequence of claim 1, further comprising base substitutions at one or more positions selected from the group consisting of positions 1633, 1666 and 2078.

43. (New) The variant determined according to the method of claim 9, further comprising a base substitution at one or more positions selected from the group consisting of positions 1633, 1666 and 2078.

REMARKS

Election of Group II With Traverse

Applicants elect Group II having claims 9-23 and 31 for further prosecution.